

SEQUENCE LISTING

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<110>	Zur Megede, Jan
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	Engelbrecht, Susan
	van Rensburg, Estrelita Janse
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<213> Artificial

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<213> Artificial

<220>

<223> synthetic Env common region of HIV strain AF110975

<400> 11

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<210> 12

<211> 1437

<212> DNA

<213> Artificial

<220>								
<223>	synthetic	gp120	coding	region	of	HIV	strain	AF110975

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<210> 13

<211> 1950

<212> DNA

<213> Artificial

<220>
<223> synthetic gp140 coding region of HIV strain AF110975

<400> 13 agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60 agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120 180 tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240 atcagectgt gggaccagag cetgaageee egegtgaage tgaceeeeet gtgegtgaee 300 360 ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 420 aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480 agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540 gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600 660 tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 720 acccacggca tcaagcccgt ggtgagcacc ccctgctgc tgaacggcag cctggccgag 780 ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 840 cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900 960 caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 1020 aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1080 ctggagatca ccacccacag cttcaactgc cgcggcgagt tcttctactg caacaccagc aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140 1200 atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc gccatctacg cccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260 ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatettccg cccccagggc 1320 ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380 cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgcgcc 1440 1500 gtgggcatcg gcgccgtgat cttcggcttc ctgggcgccg ccggcagcaa catgggcgcc 1560 gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag

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<210> 14

<211> 2493

<212> DNA

<213> Artificial

<220>

<223> synthetic gp160 coding region of HIV strain AF110975

<400> 14 agcggcctgg

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<210> 15

<211> 2565

<212> DNA

<213> Artificial

<220>
<223> synthetic signal sequence and gp160 coding region of HIV strain AF110975

<400> 15 atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60 ttctggatct gcagcggcct gggcaacctg tgggtgaccg tgtacgacgg cgtgcccgtg 120 tggcgcgagg ccagcaccac cctgttctgc gccagcgacg ccaaggccta cgagaaggag 180 gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagatc 240 gagctggaca acgtgaccga gaacttcaac atgtggaaga acgacatggt ggaccagatg 300 360 cacgaggaca tcatcagcct gtgggaccag agcctgaagc cccgcgtgaa gctgaccccc ctgtgcgtga ccctgaagtg caccaactac agcaccaact acagcaacac catgaacgcc 420 480 accagctaca acaacaacac caccgaggag atcaagaact gcaccttcaa catgaccacc gagetgegeg acaagaagca geaggtgtac geeetgttet acaagetgga categtgeee 540 600 ctgaacagca acagcagcga gtaccgcctg atcaactgca acaccagcgc catcacccag gcctgcccca aggtgagctt cgaccccatc cccatccact actgcgcccc cgccggctac 660 gccatcctga agtgcaagaa caacaccagc aacggcaccg gcccctgcca gaacgtgagc 720 780 accgtgcagt gcacccacgg catcaagccc gtggtgagca ccccctgct gctgaacggc 840 agcctggccg agggcggcga gatcatcatc cgcagcaaga acctgagcaa caacgcctac 900 accatcatcg tgcacctgaa cgacagcgtg gagatcgtgt gcacccgccc caacaacaac 960 accegeaagg geateegeat eggeeeegge cagacettet acgeeacega gaacateate 1020 ggcgacatcc gccaggccca ctgcaacatc agcgccggcg agtggaacaa ggccgtgcag 1080 1140 ageggeggeg acetggagat caccacccac agetteaact geegeggega gttettetae 1200 tgcaacacca gcaagctgtt caacagcagc tacaacggca ccagctaccg cggcaccgag agcaacagca gcatcatcac cctgccctgc cgcatcaagc agatcatcga catgtggcag 1260 aaggtgggcc gcgccatcta cgccccccc atcgagggca acatcacctg cagcagcagc 1320 atcaccggcc tgctgctggc ccgcgacggc ggcctggaca acatcaccac cgagatcttc 1380 cgcccccagg gcggcgacat gaaggacaac tggcgcaacg agctgtacaa gtacaaggtg 1440 gtggagatca agcccctggg cgtggccccc accgaggcca agcgccgcgt ggtggagcgc 1500 gagaagegeg cegtgggeat eggegeegtg atettegget teetgggege egeeggeage 1560

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<212> DNA

<213> Artificial

<220>

<223> synthetic a gp41 coding region of HIV strain AF110975

<400> 16

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<210> 17

<211> 492

<212> PRT

<213> Human immunodeficiency virus

<400> 17

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Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys 20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu 50 60

His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
100 105 110

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Asn	Tyr 130	Pro	Ile	Val	Gln	Asn 135	Leu	Gln	Gly	Gln	Met 140	Val	His	Gln	Ala
Ile 145	Ser	Pro	Arg	Thr	Leu 150	Asn	Ala	Trp	Val	Lys 155	Val	Ile	Glu	Glu	Lys 160
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Glu 305	Gln	Ser	Thr	Gln	Glu 310	Val	Lys	Asn	Trp	Met 315	Thr	Asp	Thr	Leu	Leu 320
Val	Gln	Asn	Ala	Asn 325	Pro	Asp	Cys	Lys	Thr 330	Ile	Leu	Arg	Ala	Leu 335	Gly

Pro	Gly	Ala	Ser 340	Leu	Glu	Glu	Met	Met 345	Thr	Ala	Cys	Gln	Gly 350	Val	Gly	
Gly	Pro	Ser 355	His	Lys	Ala	Arg	Val 360	Leu	Ala	Glu	Ala	Met 365	Ser	Gln	Ala	
Asn	Thr 370	Ser	Val	Met	Met	Gln 375	Lys	Ser	Asn	Phe	Lys 380	Gly	Pro	Arg	Arg	
Ile 385	Val	Lys	Cys	Phe	Asn 390	Cys	Gly	Lys	Glu	Gly 395	His	Ile	Ala	Arg	Asn 400	
Cys	Arg	Ala	Pro	Arg 405	Lys	Lys	Gly	Cys	Trp 410	Lys	Cys	Gly	Lys	Glu 415	Gly	
His	Gln	Met	Lys 420	Asp	Cys	Thr	Glu	Arg 425	Gln	Ala	Asn	Phe	Leu 430	Gly	Lys	
Ile	Trp	Pro 435	Ser	His	Lys	Gly	Arg 440	Pro	Gly	Asn	Phe	Leu 445	Gln	Ser	Arg	
Pro	Glu 450	Pro	Thr	Ala	Pro	Pro 455	Ala	Glu	Ser	Phe	Arg 460	Phe	Glu	Glu	Thr	
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<211> 1509

<212> DNA

<213> Artificial

<220>

<223> synthetic Gag coding sequence of HIV strain AF110967

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cccgccgaga	gcttccgctt	cgaggagacc	acccccgccc	ccaagcagga	gcccaaggac	1440
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<211> 502

<212> PRT

<213> Human immunodeficiency virus

<400> 22

Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys 20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro $35 \hspace{1cm} 40 \hspace{1cm} 45$

Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu $50 \hspace{1cm} 55 \hspace{1cm} 60 \hspace{1cm}$

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Tyr Asn 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Gly Ile Glu Val Arg Asp 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
100 105 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn 115 120 125

Tyr	Pro 130	Ile	Val	Gln	Asn	Leu 135	Gln	Gly	Gln	Met	Val 140	His	Gln	Ala	Ile
Ser 145	Pro	Arg	Thr	Leu	Asn 150	Ala	Trp	Val	Lys	Val 155	Ile	Glu	Glu	Lys	Ala 160
Phe	Ser	Pro	Glu	Val 165	Ile	Pro	Met	Phe	Thr 170	Ala	Leu	Ser	Glu	Gly 175	Ala
Thr	Pro	Gln	Asp 180	Leu	Asn	Thr	Met	Leu 185	Asn	Thr	Val	Gly	Gly 190	His	Gln
Ala	Ala	Met 195	Gln	Met	Leu	Lys	Asp 200	Thr	Ile	Asn	Glu	Glu 205	Ala	Ala	Glu
Trp	Asp 210	Arg	Leu	His	Pro	Val 215	Gln	Ala	Gly	Pro	Val 220	Ala	Pro	Gly	Gln
Met 225	Arg	Asp	Pro	Arg	Gly 230	Ser	Asp	Ile	Ala	Gly 235	Ala	Thr	Ser	Thr	Leu 240
Gln	Glu	Gln	Ile	Ala 245	Trp	Met	Thr	Ser	Asn 250	Pro	Pro	Val	Pro	Val 255	Gly
Asp	Ile	Tyr	Lys 260	Arg	Trp	Ile	Ile	Leu 265	Gly	Leu	Asn	Lys	Ile 270	Val	Arg
Met	Tyr	Ser 275	Pro	Val	Ser	Ile	Leu 280	Asp	Ile	Arg	Gln	Gly 285	Pro	Lys	Glu
Pro	Phe 290	Arg	Asp	Tyr	Val	Asp 295	Arg	Phe	Phe	Lys	Thr 300	Leu	Arg	Ala	Glu
Gln 305	Ala	Thr	Gln	Asp	Val 310	Lys	Asn	Trp	Met	Thr 315	Glu	Thr	Leu	Leu	Val 320
Gln	Asn	Ala	Asn	Pro 325	Asp	Cys	Lys	Thr	Ile 330	Leu	Arg	Ala	Leu	Gly 335	Pro
Gly	Ala	Thr	Leu 340	Glu	Glu	Met	Met	Thr 345	Ala	Cys	Gln	Gly	Val 350	Gly	Gly

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala Asn Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly Ser Gly Pro Leu Ser Gln <210> 23 <211> 849 <212> PRT <213> Human immunodeficiency virus <400> 23 Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn

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35 40 45

Thr	Thr 50	Leu	Phe	Суѕ	Thr	Ser 55	Asp	Ala	Lys	Ala	Tyr 60	Glu	Thr	Glu	Val
His 65	Asn	Val	Trp	Ala	Thr 70	His	Ala	Cys	Val	Pro 75	Thr	Asp	Pro	Asn	Pro 80

- Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys 85 90 95
- Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp 100 105 110
- Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu 115 120 125
- Lys Cys Arg Asn Val Asn Ala Thr Asn Asn Ile Asn Ser Met Ile Asp 130 135 140
- Asn Ser Asn Lys Gly Glu Met Lys Asn Cys Ser Phe Asn Val Thr Thr 145 150 155 160
- Glu Leu Arg Asp Arg Lys Gln Glu Val His Ala Leu Phe Tyr Arg Leu 165 170 175
- Asp Val Val Pro Leu Gln Gly Asn Asn Ser Asn Glu Tyr Arg Leu Ile 180 185 190
- Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe 195 200 205
- Asp Pro Ile Pro Ile His Tyr Cys Thr Pro Ala Gly Tyr Ala Ile Leu 210 215 220
- Lys Cys Asn Asn Gln Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val 225 230 235 240
- Ser Ser Val Gln Cys Ala His Gly Ile Lys Pro Val Val Ser Thr Gln 245 250 255
- Leu Leu Leu Asn Gly Ser Leu Ala Lys Gly Glu Ile Ile Ile Arg Ser 260 265 270

Glu	Asn	Leu 275	Ala	Asn	Asn	Ala	Lys 280	Ile	Ile	Ile	Val	Gln 285	Leu	Asn	Lys
Pro	Val 290	Lys	Ile	Val	Cys	Val 295	Arg	Pro	Asn	Asn	Asn 300	Thr	Arg	Lys	Ser
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Gly	Asp	Ile	Arg	Gln 325	Ala	Tyr	Cys	Ile	Ile 330	Asn	Lys	Thr	Glu	Trp 335	Asn
Ser	Thr	Leu	Gln 340	Gly	Val	Ser	Lys	Lys 345	Leu	Glu	Glu	His	Phe 350	Ser	Lys
Lys	Ala	Ile 355	Lys	Phe	Glu	Pro	Ser 360	Ser	Gly	Gly	Asp	Leu 365	Glu	Ile	Thr
Thr	His 370	Ser	Phe	Asn	Cys	Arg 375	Gly	Glu	Phe	Phe	Tyr 380	Cys	Asp	Thr	Ser
Gln 385	Leu	Phe	Asn	Ser	Thr 390	Tyr	Ser	Pro	Ser	Phe 395	Asn	Gly	Thr	Glu	Asn 400
Lys	Leu	Asn	Gly	Thr 405	Ile	Thr	Ile	Thr	Cys 410	Arg	Ile	Lys	Gln	Ile 415	Ile
Asn	Met	Trp	Gln 420	Lys	Val	Gly	Arg	Ala 425	Met	Tyr	Ala	Pro	Pro 430	Ile	Ala
Gly	Asn	Leu 435	Thr	Cys	Glu	Ser	Asn 440	Ile	Thr	Gly	Leu	Leu 445	Leu	Thr	Arg
Asp	Gly 450	Gly	Lys	Thr	Gly	Pro 455	Asn	Asp	Thr	Glu	Ile 460	Phe	Arg	Pro	Gly
Gly 465	Gly	Asp	Met	Arg	Asp 470	Asn	Trp	Arg	Asn	Glu 475	Leu	Tyr	Lys	Tyr	Lys 480
Val	Val	Glu	Ile	Lys 485	Pro	Leu	Gly	Val	Ala 490	Pro	Thr	Glu	Ala	Lys 495	Arg

Arg	Val	Val	Glu 500	Arg	Glu	Lys	Arg	Ala 505	Val	Gly	Ile	Gly	Ala 510	Val	Phe
Leu	Gly	Phe 515	Leu	Gly	Ala	Ala	Gly 520	Ser	Thr	Met	Gly	Ala 525	Ala	Ser	Ile
Thr	Leu 530	Thr	Val	Gln	Ala	Arg 535	Leu	Leu	Leu	Ser	Gly 540	Ile	Val	Gln	Gln
Gln 545	Asn	Asn	Leu	Leu	Arg 550	Ala	Ile	Glu	Ala	Gln 555	Gln	His	Leu	Leu	Gln 560
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Glu	Arg	Tyr	Leu 580	Lys	Asp	Gln	Gln	Leu 585	Leu	Gly	Ile	Trp	Gly 590	Cys	Ser
Gly	Lys	Leu 595	Ile	Cys	Thr	Thr	Ala 600	Val	Pro	Trp	Asn	Ser 605	Ser	Trp	Ser
Asn	Arg 610	Ser	His	Asp	Glu	Ile 615	Trp	Asp	Asn	Met	Thr 620	Trp	Met	Gln	Trp
Asp 625	Arg	Glu	Ile	Asn	Asn 630	Tyr	Thr	Asp	Thr	Ile 635	Tyr	Arg	Leu	Leu	Glu 640
Glu	Ser	Gln	Asn	Gln 645	Gln	Glu	Lys	Asn	Glu 650	Lys	Asp	Leu	Leu	Ala 655	Leu
Asp	Ser	Trp	Gln 660	Asn	Leu	Trp	Asn	Trp 665	Phe	Ser	Ile	Thr	Asn 670	Trp	Leu
Trp	Tyr	Ile 675	Lys	Ile	Phe	Ile	Met 680	Ile	Val	Gly	Gly	Leu 685	Ile	Gly	Leu
Arg	Ile 690	Ile	Phe	Ala	Val	Leu 695	Ser	Ile	Val	Asn	Arg 700	Val	Arg	Gln	Gly
Tyr 705	Ser	Pro	Leu	Pro	Phe	Gln	Thr	Leu	Thr	Pro 715	Asn	Pro	Arg	Glu	Pro 720

Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Glu Gln Asp Arg Gly 725 730 735 Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile 760 Leu Ile Ala Ala Arg Val Leu Glu Leu Gly Gln Arg Gly Trp Glu 770 775 780 Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu 790 795 Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala 805 810 815 Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala 820 825 830 Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu 840 Gln <210> 24 <211> 855 <212> PRT <213> Human immunodeficiency virus <400> 24 Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp 10 Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val 20 25

Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val

40

55

35

50

45

Trp 65	Ala	Thr	His	Ala	Cys 70	Val	Pro	Thr	Asp	Pro 75	Asn	Pro	Gln	Glu	Ile 80
Glu	Leu	Asp	Asn	Val 85	Thr	Glu	Asn	Phe	Asn 90	Met	Trp	Lys	Asn	Asp 95	Met
Val	Asp	Gln	Met 100	His	Glu	Asp	Ile	Ile 105	Ser	Leu	Trp	Asp	Gln 110	Ser	Leu
Lys	Pro	Arg 115	Val	Lys	Leu	Thr	Pro 120	Leu	Cys	Val	Thr	Leu 125	Lys	Cys	Thr
Asn	Tyr 130	Ser	Thr	Asn	Tyr	Ser 135	Asn	Thr	Met	Asn	Ala 140	Thr	Ser	Tyr	Asn
Asn 145	Asn	Thr	Thr	Glu	Glu 150	Ile	Lys	Asn	Cys	Thr 155	Phe	Asn	Met	Thr	Thr 160
Glu	Leu	Arg	Asp	Lys 165	Lys	Gln	Gln	Val	Tyr 170	Ala	Leu	Phe	Tyr	Lys 175	Leu
Asp	Ile	Val	Pro 180	Leu	Asn	Ser	Asn	Ser 185	Ser	Glu	Tyr	Arg	Leu 190	Ile	Asn
Cys	Asn	Thr 195	Ser	Ala	Ile	Thr	Gln 200	Ala	Cys	Pro	Lys	Val 205	Ser	Phe	Asp
Pro	Ile 210	Pro	Ile	His	Tyr	Cys 215	Ala	Pro	Ala	Gly	Tyr 220	Ala	Ile	Leu	Lys
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Thr	Val	Gln	Cys	Thr 245	His	Gly	Ile	Lys	Pro 250	Val	Val	Ser	Thr	Pro 255	Leu
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Lys	Asn	Leu 275	Ser	Asn	Asn	Ala	Tyr 280	Thr	Ile	Ile	Val	His 285	Leu	Asn	Asp

Ser	Val 290	Glu	Ile	Val	Cys	Thr 295	Arg	Pro	Asn	Asn	Asn 300	Thr	Arg	Lys	Gly
Ile 305	Arg	Ile	Gly	Pro	Gly 310	Gln	Thr	Phe	Tyr	Ala 315	Thr	Glu	Asn	Ile	Ile 320
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Thr	His 370	Ser	Phe	Asn	Cys	Arg 375	Gly	Glu	Phe	Phe	Туг 380	Cys	Asn	Thr	Ser
Lys 385	Leu	Phe	Asn	Ser	Ser 390	Tyr	Asn	Gly	Thr	Ser 395	Tyr	Arg	Gly	Thr	Glu 400
Ser	Asn	Ser	Ser	Ile 405	Ile	Thr	Leu	Pro	Cys 410	Arg	Ile	Lys	Gln	Ile 415	Ile
Asp	Met	Trp	Gln 420	Lys	Val	Gly	Arg	Ala 425	Ile	Tyr	Ala	Pro	Pro 430	Ile	Glu
Gly	Asn	Ile 435	Thr	Cys	Ser	Ser	Ser 440	Ile	Thr	Gly	Leu	Leu 445	Leu	Ala	Arg
Asp	Gly 450	Gly	Leu	Asp	Asn	Ile 455	Thr	Thr	Glu	Ile	Phe 460	Arg	Pro	Gln	Gly
Gly 465	Asp	Met	Lys	Asp	Asn 470	Trp	Arg	Asn	Glu	Leu 475	Tyr	Lys	Tyr	Lys	Val 480
Val	Glu	Ile	Lys	Pro 485	Leu	Gly	Val	Ala	Pro 490	Thr	Glu	Ala	Lys	Arg 495	Arg
Val	Val	Glu	Arg 500	Glu	Lys	Arg	Ala	Val 505	Gly	Ile	Gly	Ala	Val 510	Ile	Phe

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Ser 545	Asn	Leu	Leu	Arg	Ala 550	Ile	Glu	Ala	Gln	Gln 555	His	Met	Leu	Gln	Leu 560
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Lys 625	Glu	Ile	Ser	Asn	Tyr 630	Thr	Gly	Ile	Ile	Tyr 635	Arg	Leu	Leu	Glu	Glu 640
Ser	Gln	Asn	Gln	Gln 645	Glu	Gln	Asn	Glu	Lys 650	Asp	Leu	Leu	Ala	Leu 655	Asp
Ser	Arg	Asn	Asn 660	Leu	Trp	Ser	Trp	Phe 665	Asn	Ile	Ser	Asn	Trp 670	Leu	Trp
Tyr	Ile	Lys 675	Ile	Phe	Ile	Met	Ile 680	Val	Gly	Gly	Leu	Ile 685	Gly	Leu	Arg
Ile	Ile 690	Phe	Ala	Val	Leu	Ser 695	Ile	Val	Asn	Arg	Val 700	Arg	Gln	Gly	Tyr
Ser 705	Pro	Leu	Ser	Phe	Gln 710	Thr	Leu	Thr	Pro	Asn 715	Pro	Arg	Gly	Leu	Asp 720
Arg	Leu	Gly	Arg	Ile 725	Glu	Glu	Glu	Gly	Gly 730	Glu	Gln	Asp	Arg	Asp 735	Arg
Ser	Ile	Arg	Leu	Val	Gln	Gly	Phe	Leu	Ala	Leu	Ala	Trp	Asp	Asp	Leu

740 745 750

Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu 755 760 765

Val Thr Ala Arg Val Val Glu Leu Leu Gly Arg Ser Ser Pro Arg Gly 770 780

Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln 785 790 795 800

Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser 805 810 815

Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile 820 825 830

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Gly Phe Glu Ala Ala Leu Gln 850 855

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<212> PRT

<213> Human immunodeficiency virus

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Phe Phe Lys Thr 20

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<212> DNA

<213> Human immunodeficiency virus

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<223> HIV Type C Gag Wild Type

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<210> 57

<211> 624

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600

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300

354

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<223> HIV Type C Pol Wild Type

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<211> 297

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<213> Artificial

<220>

<223> HIV Type C Protease Optimized

<400> 64

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<210> 65

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<212> DNA
<213> Artificial
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<223> HIV Type C Protease Wild Type
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                                                                     120
aaatggaaac caaaaatgat agggggaatt ggaggtttta tcaaagtaag acagtatgat
                                                                     180
caaatactta tagaaatttg tggaaaaaag gctataggta cagtattagt agggcctaca
                                                                     240
                                                                     297
ccagtcaaca taattggaag aaatctgtta actcagcttg gatgcacact aaatttt
<210> 66
<211>
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<212> DNA
<213> Artificial
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<223> HIV Type C Inactivated Protease Optimized
<400> 66
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aagtggaagc ccaagatgat cggcggcatc ggcggcttca tcaaggtgcg ccagtacgac
                                                                     180
                                                                     240
cagatcctga tcgagatctg cggcaagaag gccatcggca ccgtgctggt gggcccacc
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                                                                     297
<210>
       67
<211>
       297
<212> DNA
<213> Artificial
<220>
<223> HIV Type C Inactivated Protease Wild Type
<400>
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                                                                     120
aaatggaaac caaaaatgat agggggaatt ggaggtttta tcaaagtaag acagtatgat
                                                                     180
                                                                     240
caaatactta tagaaatttg tggaaaaaag gctataggta cagtattagt agggcctaca
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- <210> 68
- <211> 1965
- <212> DNA
- <213> Artificial

<220>

<223> HIV Type C Inactivated Protease Mutated Reverse Transcriptase Optimized

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<210> 69

<211> 1965

<212> DNA

<213> Artificial

<220>

<223> HIV Type C Inactivated Protease Mutated Reverse Transcriptase Wild Type

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- <210> 70
- <211> 1977
- <212> DNA
- <213> Artificial
- <220>
- <223> HIV Type C Protease and Reverse Transcriptase Optimized
- <400> 70
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cagatectga tegagatetg eggeaagaag gecateggea eegtgetggt gggeeeeace 240 cccgtgaaca tcatcggccg caacctgctg acccagctgg gctgcaccct gaacttcccc 300 atcagcccca tcgagaccgt gcccgtgaag ctgaagcccg gcatggacgg ccccaaggtg 360 aagcagtggc ccctgaccga ggagaagatc aaggccctga ccgccatctg cgaggagatg 420 gagaaggagg gcaagatcac caagatcggc cccgacaacc cctacaacac ccccgtgttc 480 gccatcaaga agaaggacag caccaagtgg cgcaagctgg tggacttccg cgagctgaac 540 aagcgcaccc aggacttctg ggaggtgcag ctgggcatcc cccaccccgc cggcctgaag 600 aagaagaaga gcgtgaccgt gctggacgtg ggcgacgcct acttcagcgt gcccctggac 660 720 gagagettee geaagtacae egeetteace atececagea teaacaaega gaeeeeegge 780 atccgctacc agtacaacgt gctgccccag ggctggaagg gcagccccgc catcttccag agcagcatga ccaagatcct ggagcccttc cgcgccaaga accccgacat cgtgatctac 840 cagtacatgg acgacctgta cgtgggcagc gacctggaga tcggccagca ccgcgccaag 900 atcgaggagc tgcgcgagca cctgctgaag tggggcttca ccacccccga caagaagcac 960 1020 cagaaggagc ccccttcct gtggatgggc tacgagctgc accccgacaa gtggaccgtg cageceatee tgetgeeega gaaggacage tggacegtga acgaeateea gaagetggtg 1080 1140 ggcaagctga actgggccag ccagatctac cccggcatca aggtgcgcca gctgtgcaag ctgctgcgcg gcgccaaggc cctgaccgac atcgtgcccc tgaccgagga ggccgagctg 1200 1260 gagctggccg agaaccgcga gatcctgcgc gagcccgtgc acggcgtgta ctacgacccc agcaaggacc tgatcgccga gatccagaag cagggccacg agcagtggac ctaccagatc 1320 1380 taccaggage cetteaagaa eetgaagaee ggeaagtaeg ecaagatgeg caccacceae 1440 accaacgacg tgaagcagct gaccgaggcc gtgcagaaga tcgccatgga gagcatcgtg 1500 atctggggca agacccccaa gttccgcctg cccatccaga aggagacctg ggagacctgg 1560 tggaccgact actggcaggc cacctggatc cccgagtggg agttcgtgaa caccccccc 1620 ctggtgaagc tgtggtacca gctggagaag gaccccatcg ccggcgtgga gaccttctac gtggacggcg ccaccaaccg cgaggccaag atcggcaagg ccggctacgt gaccgaccgc 1680 ggccgccaga agatcgtgac cctgaccaac accaccaacc agaagaccga gctgcaggcc 1740 1800 atccagctgg ccctgcagga cagcggcagc gaggtgaaca tcgtgaccga cagccagtac 1860 gccctgggca tcatccaggc ccagcccgac aagagcgaca gcgagatctt caaccagatc atcgagcagc tgatcaacaa ggagcgcatc tacctgagct gggtgcccgc ccacaagggc 1920

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<210> 71 <211> 1977 <212> DNA <213> Artificial					
<220> <223> HIV Type C Pro	tease and Re	everse Trans	scriptase W	ild Type	
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aaatggaaac caaaaatgat	agggggaatt	ggaggtttta	tcaaagtaag	acagtatgat	180
caaatactta tagaaatttg	tggaaaaaag	gctataggta	cagtattagt	agggcctaca	240
ccagtcaaca taattggaag	aaatctgtta	actcagcttg	gatgcacact	aaattttcca	300
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aagaaaaaat cagtgacagt	gctagatgtg	ggggatgcat	atttttcagt	tcctttagat	660
gaaagcttca ggaaatatac	tgcattcacc	atacctagta	taaacaatga	aacaccaggg	720
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caatatatgg atgacttgta	tgtaggatct	gacttagaaa	tagggcaaca	tagagcaaaa	900
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gaattggcag agaacaggga	aattttaaga	gaaccagtac	atggagtata	ttatgatcca	1260
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tatcaag	aac	catttaaaaa	tctgaaaaca	gggaagtatg	caaaaatgag	gactacccac	1380
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atatggg	gaa	agactcctaa	atttagacta	cccatccaaa	aagaaacatg	ggagacatgg	1500
tggacag	act	attggcaagc	cacctggatc	cctgagtggg	agtttgttaa	tacccctccc	1560
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ggaaggc	aga	aaattgttac	tctaactaac	acaacaaatc	agaagactga	gttacaagca	1740
attcagc	tag	ctctgcagga	ttcaggatca	gaagtaaaca	tagtaacaga	ctcacagtat	1800
gcattag	gaa	tcattcaagc	acaaccagat	aagagtgact	cagagatatt	taaccaaata	1860
atagaac	agt	taataaacaa	ggaaagaatc	tacctgtcat	gggtaccagc	acataaagga	1920
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	72 gcc	gcagcggcga	cagcgacgag	gccctgctgc	aggtggtgaa	gatcatcaag	60
atcctgt	acc	agagc				,	75
<211> <212>	73 76 DNA Arti	ficial					
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	73 gaa	gaagcggaga	cagcgacgaa	gcgctcctcc	aagtggtgaa	gatcatcaaa	60
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<211>	74 246 DNA						

75

<213> Artificial

<220>

<223> HIV Type C RevExon2 Optimized	
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agegeegage eegtgeeeet geagetgeee eecetggage geetgeacat caactgeage	180
gagggcagcg gcaccagcgg cacccagcag agccagggca ccaccgaggg cgtgggcgac	240
ccctaa	246
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gatctgcgga gcctgtgcct cttcagctac caccgcttga gagacttcat attaattgca	180
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atccttaa	248
<210> 76 <211> 1680 <212> DNA <213> Artificial	
<220> <223> HIV Type C Reverse Transcriptase Optimized	
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atggagaagg agggcaagat caccaagatc ggccccgaca acccctacaa caccccgtg	180
ttcgccatca agaagaagga cagcaccaag tggcgcaagc tggtggactt ccgcgagctg	240
aacaagcgca cccaggactt ctgggaggtg cagctgggca tcccccaccc cgccggcctg	300
aagaagaaga agagcgtgac cgtgctggac gtgggcgacg cctacttcag cgtgcccctg	360
gacgagaget teegeaagta caeegeette aecateeeca geateaacaa egagaeeece	420

480 ggcatccgct accagtacaa cgtgctgccc cagggctgga agggcagccc cgccatcttc cagagcagca tgaccaagat cctggagccc ttccgcgcca agaaccccga catcgtgatc 540 taccagtaca tggacgacct gtacgtgggc agcgacctgg agatcggcca gcaccgcgcc 600 aagatcgagg agctgcgcga gcacctgctg aagtggggct tcaccacccc cgacaagaag 660 720 caccagaagg agccccctt cctgtggatg ggctacgagc tgcaccccga caagtggacc 780 gtgcagccca tcctgctgcc cgagaaggac agctggaccg tgaacgacat ccagaagctg gtgggcaagc tgaactgggc cagccagatc taccccggca tcaaggtgcg ccagctgtgc 840 900 aagctgctgc gcggcgccaa ggccctgacc gacatcgtgc ccctgaccga ggaggccgag 960 ctggagctgg ccgagaaccg cgagatcctg cgcgagcccg tgcacggcgt gtactacgac 1020 cccagcaagg acctgatcgc cgagatccag aagcagggcc acgagcagtg gacctaccag 1080 atctaccagg agcccttcaa gaacctgaag accggcaagt acgccaagat gcgcaccacc 1140 cacaccaacg acgtgaagca gctgaccgag gccgtgcaga agatcgccat ggagagcatc 1200 gtgatctggg gcaagacccc caagttccgc ctgcccatcc agaaggagac ctgggagacc tggtggaccg actactggca ggccacctgg atccccgagt gggagttcgt gaacaccccc 1260 1320 cccctggtga agctgtggta ccagctggag aaggacccca tcgccggcgt ggagaccttc 1380 tacgtggacg gcgccaccaa ccgcgaggcc aagatcggca aggccggcta cgtgaccgac 1440 cgcggccgcc agaagatcgt gaccctgacc aacaccacca accagaagac cgagctgcag 1500 gccatccagc tggccctgca ggacagcggc agcgaggtga acatcgtgac cgacagccag 1560 tacgccctgg gcatcatcca ggcccagccc gacaagagcg acagcgagat cttcaaccag 1620 atcatcgagc agctgatcaa caaggagcgc atctacctga gctgggtgcc cgcccacaag 1680 ggcatcggcg gcaacgagca ggtggacaag ctggtgagca agggcatccg caaggtgctg

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<210> 77

<211> 1680

<212> DNA

<213> Artificial

<220>

<223> HIV Type C Reverse Transcriptase Wild Type

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aaaaagaaaa	aatcagtgac	agtgctagat	gtgggggatg	catattttc	agttccttta	360
gatgaaagct	tcaggaaata	tactgcattc	accataccta	gtataaacaa	tgaaacacca	420
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cccacca	aagc	ccgtgcccct	gctgctgccc	cccatcgagc	gcctgcacat	caactgcagc	180
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1380

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Ala Val Phe Val Ser Pro Ser 20

115

125

120

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	Gly 370	Gly	Glu	Phe		Tyr 375	_	Asn	Ser	Thr	Gln 380	Leu	Phe	Asn	Ser
mb	Ф.	3 ~~	3 ~ ~	mb	т1.	Q1	Desa	3	3 ~~	mb	7 ~~	01	Ωla se	T1.	Ωb ••

360

355

365

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Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly 405 410 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser 420 425 430

Asn Ile Thr Gly Leu Leu Thr Arg Asp Gly Gly Lys Glu Ile Ser 435 440 445

Asn Thr Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn 450 455 460

Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu 465 470 475 480

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys 485 490 495

Arg Ala Val Thr Leu Gly Ala Met Phe Leu Gly Phe Leu Gly Ala Ala 500 505 510

Gly Ser Thr Met Gly Ala Arg Ser Leu Thr Leu Thr Val Gln Ala Arg 515 520 525

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala 530 535 540

Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys 545 550 555 560

Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln 565 570 575

Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr 580 585 590

Ala	Val	Pro 595	Trp	Asn	Ala	Ser	Trp 600	Ser	Asn	Lys	Ser	Leu 605	Asp	Gln	Ile
Trp	Asn 610	Asn	Met	Thr	Trp	Met 615	Glu	Trp	Glu	Arg	Glu 620	Ile	Asp	Asn	Tyr
Thr 625	Asn	Leu	Ile	Tyr	Thr 630	Leu	Ile	Glu	Glu	Ser 635	Gln	Asn	Gln	Gln	Glu 640
Lys	Asn	Glu	Gln	Glu 645	Leu	Leu	Glu	Leu	Asp 650	Lys	Trp	Ala	Ser	Leu 655	Trp
Asn	Trp	Phe	Asp 660	Ile	Ser	Lys	Trp	Leu 665	Trp	Tyr	Ile	Lys	Ile 670	Phe	Ile
Met	Ile	Val 675	Gly	Gly	Leu	Val	Gly 680	Leu	Arg	Ile	Val	Phe 685	Thr	Val	Leu
Ser	Ile 690	Val	Asn	Arg	Val	Arg 695	Gln	Gly	Tyr	Ser	Pro 700	Leu	Ser	Phe	Gln
Thr 705	Arg	Phe	Pro	Ala	Pro 710	Arg	Gly	Pro	Asp	Arg 715	Pro	Glu	Gly	Ile	Glu 720
Glu	Glu	Gly	Gly	Glu 725	Arg	Asp	Arg	Asp	Arg 730	Ser	Ser	Pro	Leu	Val 735	His
Gly	Leu	Leu	Ala 740	Leu	Ile	Trp	Asp	Asp 745	Leu	Arg	Ser	Leu	Cys 750	Leu	Phe
Ser	Tyr	His 755	Arg	Leu	Arg	Asp	Leu 760	Ile	Leu	Ile	Ala	Ala 765	Arg	Ile	Val
Glu	Leu 770	Leu	Gly	Arg	Arg	Gly 775	Trp	Glu	Ala	Leu	Lys 780	Tyr	Trp	Gly	Asn
Leu 785	Leu	Gln	Tyr	Trp	Ile 790	Gln	Glu	Leu	Lys	Asn 795	Ser	Ala	Val	Ser	Leu 800
Phe	Asp	Ala	Ile	Ala 805	Ile	Ala	Val	Ala	Glu 810	Gly	Thr	Asp	Arg	Ile 815	Ile

Glu Val Ala Gln Arg Ile Gly Arg Ala Phe Leu His Ile Pro Arg Arg 820 825 830

Ile Arg Gln Gly Phe Glu Arg Ala Leu Leu 835 840

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Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val His 50 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln 65 70 75 80

Glu Ile Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn 85 90 95

Asp Met Ala Asp Gln Met His Glu Asp Val Ile Ser Leu Trp Asp Gln
100 105 110

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn 115 120 125

Cys Thr Asp Thr Asn Val Thr Gly Asn Arg Thr Val Thr Gly Asn Ser 130 140

Thr Asn Asn Thr Asn Gly Thr Gly Ile Tyr Asn Ile Glu Glu Met Lys 145 150 155 160

Asn Cys Ser Phe Asn Ala Thr Thr Glu Leu Arg Asp Lys Lys His Lys

165	170	175
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Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile His Tyr 210 215 220

Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe 225 230 235 240

Asn Gly Thr Gly Pro Cys Tyr Asn Val Ser Thr Val Gln Cys Thr His $245 \\ 250 \\ 255$

Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu 260 265 270

Ala Glu Glu Gly Ile Ile Ile Arg Ser Glu Asn Leu Thr Glu Asn Thr 275 280 285

Lys Thr Ile Ile Val His Leu Asn Glu Ser Val Glu Ile Asn Cys Thr 290 295 300

Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln 305 310 315 320

Ala Phe Tyr Ala Thr Asn Asp Val Ile Gly Asn Ile Arg Gln Ala His 325 330 335

Cys Asn Ile Ser Thr Asp Arg Trp Asn Lys Thr Leu Gln Gln Val Met 340 345 350

Lys Lys Leu Gly Glu His Phe Pro Asn Lys Thr Ile Gln Phe Lys Pro 355 360 365

His Ala Gly Gly Asp Leu Glu Ile Thr Met His Ser Phe Asn Cys Arg $370 \hspace{1cm} 375 \hspace{1cm} 380$

Gly Glu Phe Phe Tyr Cys Asn Thr Ser Asn Leu Phe Asn Ser Thr Tyr 385 390 395 400

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Val	Gly	Gln 435	Ala	Thr	Tyr	Ala	Pro 440	Pro	Ile	Ala	Gly	Asn 445	Ile	Thr	Cys
Arg	Ser 450	Asn	Ile	Thr	Gly	Ile 455	Leu	Leu	Thr	Arg	Asp 460	Gly	Gly	Phe	Asn
Thr 465	Thr	Asn	Asn	Thr	Glu 470	Thr	Phe	Arg	Pro	Gly 475	Gly	Gly	Asp	Met	Arg 480
Asp	Asn	Trp	Arg	Ser 485	Glu	Leu	Tyr	Lys	Tyr 490	Lys	Val	Val	Glu	Ile 495	Lys
Pro	Leu	Gly	Ile 500	Ala	Pro	Thr	Lys	Ala 505	Lys	Arg	Arg	Val	Val 510	Gln	Arg
Glu	Lys	Arg 515	Ala	Val	Gly	Ile	Gly 520	Ala	Val	Phe	Leu	Gly 525	Phe	Leu	Gly
Ala	Ala 530	Gly	Ser	Thr	Met	Gly 535	Ala	Ala	Ser	Ile	Thr 540	Leu	Thr	Val	Gln
Ala 545	Arg	Gln	Leu	Leu	Ser 550	Gly	Ile	Val	Gln	Gln 555	Gln	Ser	Asn	Leu	Leu 560
Lys	Ala	Ile	Glu	Ala 565	Gln	Gln	His	Met	Leu 570	Gln	Leu	Thr	Val	Trp 575	Gly
Ile	Lys	Gln	Leu 580	Gln	Ala	Arg	Val	Leu 585	Ala	Ile	Glu	Arg	Tyr 590	Leu	Lys
Asp	Gln	Gln 595	Leu	Leu	Gly	Ile	Trp 600	Gly	Cys	Ser	Gly	Arg 605	Leu	Ile	Cys
Thr	Thr 610	Ala	Val	Pro	Trp	Asn 615	Ser	Ser	Trp	Ser	Asn 620	Lys	Ser	Glu	Lys

Asp 625	Ile	Trp	Asp	Asn	Met 630	Thr	Trp	Met	Gln	Trp 635	Asp	Arg	Glu	Ile	Ser 640
Asn	Tyr	Thr	Gly	Leu 645	Ile	Tyr	Asn	Leu	Leu 650	Glu	Asp	Ser	Gln	Asn 655	Gln
Gln	Glu	Lys	Asn 660	Glu	Lys	Asp	Leu	Leu 665	Glu	Leu	Asp	Lys	Trp 670	Asn	Asn
Leu	Trp	Asn 675	Trp	Phe	Asp	Ile	Ser 680	Asn	Trp	Pro	Trp	Туг 685	Ile	Lys	Ile
Phe	Ile 690	Met	Ile	Val	Gly	Gly 695	Leu	Ile	Gly	Leu	Arg 700	Ile	Ile	Phe	Ala
Val 705	Leu	Ser	Ile	Val	Asn 710	Arg	Val	Arg	Gln	Gly 715	Tyr	Ser	Pro	Leu	Ser 720
Phe	Gln	Thr	Leu	Thr 725	Pro	Ser	Pro	Arg	Gly 730	Leu	Asp	Arg	Leu	Gly 735	Gly
Ile	Glu	Glu	Glu 740	Gly	Gly	Glu	Gln	Asp 745	Arg	Asp	Arg	Ser	Ile 750	Arg	Leu
Val	Ser	Gly 755	Phe	Leu	Ser	Leu	Ala 760	Trp	Asp	Asp	Leu	Arg 765	Asn	Leu	Cys
Leu	Phe 770	Ser	Tyr	His	Arg	Leu 775	Arg	Asp	Phe	Ile	Leu 780	Ile	Ala	Val	Arg
Ala 785	Val	Glu	Leu	Leu	Gly 790	His	Ser	Ser	Leu	Arg 795	Gly	Leu	Gln	Arg	Gly 800
Trp	Glu	Ile	Leu	Lys 805	Tyr	Leu	Gly	Ser	Leu 810	Val	Gln	Tyr	Trp	Gly 815	Leu
Glu	Leu	Lys	Lys 820	Ser	Ala	Ile	Ser	Leu 825	Leu	Asp	Thr	Ile	Ala 830	Ile	Thr
Val	Ala	Glu 835	Gly	Thr	Asp	Arg	Ile 840	Ile	Glu	Leu	Val	Gln 845	Arg	Ile	Cys

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Asn Cys Ser Phe Asn Ala Thr Thr Glu Leu Arg Asp Lys Lys His Lys

Glu	Tyr	Ala	Leu 180	Phe	Tyr	Lys	Leu	Asp 185	Ile	Val	Pro	Leu	Asn 190	Glu	Asn
Ser	Asn	Asn 195	Phe	Thr	Tyr	Arg	Leu 200	Ile	Asn	Cys	Asn	Thr 205	Ser	Thr	Ile
Thr	Gln 210	Ala	Cys	Pro	Lys	Val 215	Ser	Phe	Asp	Pro	Ile 220	Pro	Ile	His	Tyr
Cys 225	Ala	Pro	Ala	Asp	Tyr 230	Ala	Ile	Leu	Lys	Суs 235	Asn	Asn	Lys	Thr	Phe 240
Asn	Gly	Thr	Gly	Pro 245	Cys	Tyr	Asn	Val	Ser 250	Thr	Val	Gln	Cys	Thr 255	His
Gly	Ile	Lys	Pro 260	Val	Val	Ser	Thr	Gln 265	Leu	Leu	Leu	Asn	Gly 270	Ser	Leu
Ala	Glu	Glu 275	Gly	Ile	Ile	Ile	Arg 280	Ser	Glu	Asn	Leu	Thr 285	Glu	Asn	Thr
Lys	Thr 290	Ile	Ile	Val	His	Leu 295	Asn	Glu	Ser	Val	Glu 300	Ile	Asn	Cys	Thr
Arg 305	Pro	Asn	Asn	Asn	Thr 310	Arg	Lys	Ser	Val	Arg 315	Ile	Gly	Pro	Gly	Gln 320
Ala	Phe	Tyr	Ala	Thr 325	Asn	Asp	Val	Ile	Gly 330	Asn	Ile	Arg	Gln	Ala 335	His
Cys	Asn	Ile	Ser 340	Thr	Asp	Arg	Trp	Asn 345	Lys	Thr	Leu	Gln	Gln 350	Val	Met
Lys	Lys	Leu 355	Gly	Glu	His	Phe	Pro 360	Asn	Lys	Thr	Ile	Lys 365	Phe	Glu	Pro
His	Ala 370	Gly	Gly	Asp	Leu	Glu 375	Ile	Thr	Met	His	Ser 380	Phe	Asn	Cys	Arg
Gly 385	Glu	Phe	Phe	Tyr	Cys 390	Asn	Thr	Ser	Asn	Leu 395	Phe	Asn	Ser	Thr	Tyr 400

Tyr	Pro	Lys	Asn	Gly 405	Thr	Tyr	Lys	Tyr	Asn 410	Gly	Asn	Ser	Ser	Leu 415	Pro
Ile	Thr	Leu	Gln 420	Cys	Lys	Ile	Lys	Gln 425	Ile	Val	Arg	Met	Trp 430	Gln	Gly
Val	Gly	Gln 435	Ala	Met	Tyr	Ala	Pro 440	Pro	Ile	Ala	Gly	Asn 445	Ile	Thr	Cys
Arg	Ser 450	Asn	Ile	Thr	Gly	Ile 455	Leu	Leu	Thr	Arg	Asp 460	Gly	Gly	Phe	Asn
Asn 465	Thr	Asn	Asn	Asp	Thr 470	Glu	Glu	Thr	Phe	Arg 475	Pro	Gly	Gly	Gly	Asp 480
Met	Arg	Asp	Asn	Trp 485	Arg	Ser	Glu	Leu	Tyr 490	Lys	Tyr	Lys	Val	Val 495	Glu
Ile	Lys	Pro	Leu 500	Gly	Ile	Ala	Pro	Thr 505	Lys	Ala	Lys	Arg	Arg 510	Val	Val
Gln	Arg	Lys 515	Lys	Arg	Ala	Val	Gly 520	Ile	Gly	Ala	Val	Phe 525	Leu	Gly	Phe
Leu	Gly 530	Ala	Ala	Gly	Ser	Thr 535	Met	Gly	Ala	Ala	Ser 540	Ile	Thr	Leu	Thr
Val 545	Gln	Ala	Arg	Gln	Leu 550	Leu	Ser	Gly	Ile	Val 555	Gln	Gln	Gln	Ser	Asn 560
Leu	Leu	Lys	Ala	Ile 565	Glu	Ala	Gln	Gln	His 570	Met	Leu	Gln	Leu	Thr 575	Val
Trp	Gly	Ile	Lys 580	Gln	Leu	Gln	Ala	Arg 585	Val	Leu	Ala	Ile	Glu 590	Arg	Tyr
	_	595			Leu		600					605			
Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ser	Ser	Trp	Ser	Asn	Lys	Ser

625	Ala	Asp	Ile	Trp	630	Asn	Met	Thr	Trp	Met 635	GIn	Trp	Asp	Arg	640
Ile	Asn	Asn	Tyr	Thr 645	Glu	Thr	Ile	Phe	Arg 650	Leu	Leu	Glu	Asp	Ser 655	Gln
Asn	Gln	Gln	Glu 660	Lys	Asn	Glu	Lys	Asp 665	Leu	Leu	Glu	Leu	Asp 670	Lys	Trp
Asn	Asn	Leu 675	Trp	Asn	Trp	Phe	Asp 680	Ile	Ser	Asn	Trp	Leu 685	Trp	Tyr	Ile
Lys	Ile 690	Phe	Ile	Met	Ile	Val 695	Gly	Gly	Leu	Ile	Gly 700	Leu	Arg	Ile	Ile
Phe 705	Ala	Val	Leu	Ser	Ile 710	Val	Asn	Arg	Val	Arg 715	Gln	Gly	Tyr	Ser	Pro 720
Leu	Ser	Phe	Gln	Thr 725	Leu	Thr	Pro	Ser	Pro 730	Arg	Gly	Leu	Asp	Arg 735	Leu
Gly	Gly	Ile	Glu 740	Glu	Glu	Gly	Gly	Glu 745	Gln	Asp	Arg	Asp	Arg 750	Ser	Ile
Arg	Leu	Val 755	Ser	Gly	Phe	Leu	Ser 760	Leu	Ala	Trp	Asp	Asp 765	Leu	Arg	Ser
Leu	Cys 770	Leu	Phe	Ser	Tyr	His 775	Arg	Leu	Arg	Asp	Phe 780	Ile	Leu	Ile	Ala
Val 785	Arg	Ala	Val	Glu	Leu 790	Leu	Gly	His	Ser	Ser 795	Leu	Arg	Gly	Leu	Gln 800
Arg	Gly	Trp	Glu	Ile 805	Leu	Lys	Tyr	Leu	Gly 810	Ser	Leu	Val	Gln	Tyr 815	Trp
Gly	Leu	Glu	Leu 820	Lys	Lys	Ser	Ala	Ile 825	Ser	Pro	Leu	Asp	Thr 830	Ile	Ala
Ile	Ala	Val 835	Ala	Glu	Gly	Thr	Asp 840	Arg	Ile	Ile	Glu	Leu 845	Val	Gln	Arg
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Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His 50 55 60

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Glu Val Ile Leu Gly Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn 85 90 95

Asp Met Val Asp Gln Met Gln Glu Asp Ile Ile Ser Leu Trp Asp Gln
100 105 110

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn 115 120 125

Cys Thr Asn Ala Thr Val Asn Tyr Asn Asn Thr Ser Lys Asp Met Lys 130 135 140

Asn Cys Ser Phe Tyr Val Thr Thr Glu Leu Arg Asp Lys Lys Lys 145 150 155 160

Glu Asn Ala Leu Phe Tyr Arg Leu Asp Ile Val Pro Leu Asn Asn Arg 165 170 175

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Ala	Ile	Thr 195	Gln	Ala	Cys	Pro	Lys 200	Val	Ser	Phe	Asp	Pro 205	Ile	Pro	Ile
His	Tyr 210	Cys	Ala	Pro	Ala	Gly 215	Tyr	Ala	Pro	Leu	Lys 220	Cys	Asn	Asn	Lys
Lys 225	Phe	Asn	Gly	Ile	Gly 230	Pro	Cys	Asp	Asn	Val 235	Ser	Thr	Val	Gln	Cys 240
Thr	His	Gly	Ile	Lys 245	Pro	Val	Val	Ser	Thr 250	Gln	Leu	Leu	Leu	Asn 255	Gly
Ser	Leu	Ala	Glu 260	Glu	Glu	Ile	Ile	Ile 265	Arg	Ser	Glu	Asn	Leu 270	Thr	Asn
Asn	Val	Lys 275	Thr	Ile	Ile	Val	His 280	Leu	Asn	Glu	Ser	Ile 285	Glu	Ile	Lys
Cys	Thr 290	Arg	Pro	Gly	Asn	Asn 295	Thr	Arg	Lys	Ser	Val 300	Arg	Ile	Gly	Pro
Gly 305	Gln	Ala	Phe	Tyr	Ala 310	Thr	Gly	Asp	Ile	Ile 315	Gly	Asp	Ile	Arg	Gln 320
Ala	His	Cys	Asn	Ile 325	Ser	Lys	Asn	Glu	Trp 330	Asn	Thr	Thr	Leu	Gln 335	Arg
Val	Ser	Gln	Lys 340	Leu	Gln	Glu	Leu	Phe 345	Pro	Asn	Ser	Thr	Gly 350	Ile	Lys
Phe	Ala	Pro 355	His	Ser	Gly	Gly	Asp 360	Leu	Glu	Ile	Thr	Thr 365	His	Ser	Phe
Asn	Cys 370	Gly	Gly	Glu	Phe	Phe 375	Tyr	Cys	Asn	Thr	Thr 380	Asp	Leu	Phe	Asn
Ser 385	Thr	Tyr	Ser	Asn	Gly 390	Thr	Cys	Thr	Asn	Gly 395	Thr	Cys	Met	Ser	Asn 400

Asn	Thr	Glu	Arg	Ile 405	Thr	Leu	Gln	Cys	Arg 410	Ile	Lys	Gln	Ile	Ile 415	Asn
Met	Trp	Gln	Glu 420	Val	Gly	Arg	Ala	Met 425	Tyr	Ala	Pro	Pro	Ile 430	Ala	Gly
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Gly	Gly 450	Asp	Asn	Asn	Thr	Glu 455	Thr	Glu	Thr	Phe	Arg 460	Pro	Gly	Gly	Gly
Asp 465	Met	Arg	Asp	Asn	Trp 470	Arg	Ser	Glu	Leu	Tyr 475	Lys	Tyr	Lys	Val	Val 480
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Val	Glu	Arg	Glu 500	Lys	Arg	Ala	Val	Gly 505	Ile	Gly	Ala	Val	Phe 510	Leu	Gly
Phe	Leu	Gly 515	Ala	Ala	Gly	Ser	Thr 520	Met	Gly	Ala	Ala	Ser 525	Ile	Thr	Leu
Thr	Val 530	Gln	Ala	Arg	Gln	Leu 535	Leu	Ser	Gly	Ile	Val 540	Gln	Gln	Gln	Ser
Asn 545	Leu	Leu	Arg	Ala	Ile 550	Glu	Ala	Gln	Gln	His 555	Met	Leu	Gln	Leu	Thr 560
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Tyr	Leu	Gln	Asp 580	Gln	Gln	Leu	Leu	Gly 585	Leu	Trp	Gly	Cys	Ser 590	Gly	Lys
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Thr	Gln 610	Ser	Asp	Ile	Trp	Asp 615	Asn	Met	Thr	Trp	Met 620	Gln	Trp	Asp	Arg
Glu	Ile	Ser	Asn	Tyr	Thr	Asn	Thr	Ile	Tyr	Arg	Leu	Leu	Glu	Asp	Ser

Gln Ser Gln Glu Arg Asn Glu Lys Asp Leu Leu Ala Leu Asp Arg
645 650 655

Trp Asn Asn Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp Leu Trp Tyr
660 665 670

Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile 675 680 685

Ile Phe Ala Val Leu Ser Leu Val Asn Arg Val Arg Gln Gly Tyr Ser 690 695 700

Pro Leu Ser Leu Gln Thr Leu Ile Pro Asn Pro Arg Gly Pro Asp Arg 705 710 715 720

Leu Gly Gly Ile Glu Glu Gly Gly Glu Gln Asp Ser Ser Arg Ser
725 730 735

Ile Arg Leu Val Ser Gly Phe Leu Thr Leu Ala Trp Asp Asp Leu Arg 740 745 750

Ser Leu Cys Leu Phe Cys Tyr His Arg Leu Arg Asp Phe Ile Leu Ile 755 760 765

Val Val Arg Ala Val Glu Leu Leu Gly His Ser Ser Leu Arg Gly Leu 770 780

Gln Arg Gly Trp Gly Thr Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr 785 790 795 800

Trp Gly Leu Glu Leu Lys Lys Ser Ala Ile Asn Leu Leu Asp Thr Ile 805 810 815

Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Leu Glu Phe Ile Gln 820 825 830

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Trp	Val	Thr 35	Val	Tyr	Tyr	Gly	Val 40	Pro	Val	Trp	Arg	Glu 45	Ala	Lys	Thr
Thr	Leu 50	Phe	Cys	Ala	Ser	Asp 55	Ala	Lys	Ala	Tyr	Glu 60	Thr	Glu	Val	His
Asn 65	Val	Trp	Ala	Thr	His 70	Ala	Cys	Val	Pro	Thr 75	Asp	Pro	Asn	Pro	Gln 80
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Asn	Met	Val	Asp 100	Gln	Met	His	Glu	Asp 105	Ile	Ile	Ser	Leu	Trp 110	Asp	Gln
Ser	Leu	Lys 115	Pro	Cys	Val	Lys	Leu 120	Thr	Pro	Leu	Cys	Val 125	Thr	Leu	Asn
Cys	Thr 130	Asn	Thr	Asn	Val	Thr 135	Gly	Asn	Arg	Thr	Val 140	Thr	Gly	Asn	Ser
Asn 145	Ser	Asn	Xaa	Xaa	Ala 150	Xaa	Ala	Xaa	Tyr	Хаа 155	Xaa	Glu	Glu	Met	Lys 160
Asn	Cys	Ser	Phe	Asn 165	Val	Thr	Thr	Glu	Leu 170	Arg	Asp	Lys	Lys	His 175	Lys
Glu	Tyr	Ala	Leu 180	Phe	Tyr	Lys	Leu	Asp 185	Ile	Val	Pro	Leu	Asn 190	Asn	Xaa
Glu	Asn	Ser 195	Asn	Asn	Phe	Thr	Tyr 200	Arg	Leu	Ile	Asn	Cys 205	Asn	Thr	Ser
Thr	Ile 210	Thr	Gln	Ala	Cys	Pro 215	Lys	Val	Ser	Phe	Asp 220	Pro	Ile	Pro	Ile

His Tyr Cys 225	Ala Pro	Ala Gly 230	Tyr	Ala	Ile	Leu 235	Lys	Cys	Asn	Asn	Lys 240
Thr Phe Asn	Gly Thr 245	Gly Pro	Cys	Tyr	Asn 250	Val	Ser	Thr	Val	Gln 255	Cys
Thr His Gly	Ile Lys 260	Pro Val	Val	Ser 265	Thr	Gln	Leu	Leu	Leu 270	Asn	Gly
Ser Leu Ala 275		Gly Ile	Ile 280	Ile	Arg	Ser	Glu	Asn 285	Leu	Thr	Glu
Asn Thr Lys 290	Thr Ile	Ile Val 295		Leu	Asn	Glu	Ser 300	Val	Glu	Ile	Asn
Cys Thr Arg 305	Pro Asn	Asn Asn 310	Thr	Arg	Lys	Ser 315	Val	Arg	Ile	Gly	Pro 320
Gly Gln Ala	Phe Tyr 325	Ala Thr	Asn	Asp	Ile 330	Ile	Gly	Asn	Ile	Arg 335	Gln
Ala His Cys	Asn Ile 340	Ser Thr	Asp	Arg 345	Trp	Asn	Lys	Thr	Leu 350	Gln	Gln
Val Met Lys 355	Lys Leu	Gln Glu	His 360	Phe	Pro	Asn	Lys	Thr 365	Xaa	Ile	Lys
Phe Lys Pro 370	His Ala	Gly Gly 375		Leu	Glu	Ile	Thr 380	Met	His	Ser	Phe
Asn Cys Arg 385	Gly Glu	Phe Phe	Tyr	Cys	Asn	Thr 395	Ser	Asn	Leu	Phe	Asn 400
Ser Thr Tyr	His Asn 405	Xaa Xaa	Xaa	Xaa	Asn 410	Gly	Thr	Tyr	Lys	Tyr 415	Asn
Gly Asn Ser	Ser Xaa 420	Pro Ile	Thr	Leu 425	Gln	Cys	Lys	Ile	Lys 430	Gln	Ile
Ile Arg Met 435	Trp Gln	Gly Val	Gly 440	Gln	Ala	Met	Tyr	Ala 445	Pro	Pro	Ile
Ala Gly Asn	Ile Thr	Cys Arg	Ser	Asn	Ile	Thr	Gly	Ile	Leu	Leu	Thr

450 455 460

Arg Asp Gly Gly Phe Asn Asn Thr Asn Thr Xaa Xaa Thr Glu Thr Phe Arg Pro Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Ser Asn Leu Leu Lys Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Glu Ala Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asn Thr Ile Tyr Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Glu Leu Asp Lys Trp Asn Asn Leu Trp Asn Trp Phe Asp Ile Ser

Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser Pro Arg Gly Pro Asp Arg Leu Gly Gly Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ser Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile Leu Ile Ala Val Arg Ala Val Glu Leu Leu Gly His Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ile Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Leu Val Gln Arg Ile Cys Arg Ala Ile Leu Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Leu